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**Amendments to the specification:**

Please replace the paragraph at page 54, lines 3-19, with

the following:

Polypeptides of the invention may be post-translationally
modified.  Post-translational modifications include
phosphorylation of amino acid residues serine, threonine and/or
tyrosine, N-linked and/or O-linked glycosylation, methylation,
acetylation, prenylation, methylation, acetylation, arginylation,
ubiquination and racemization.  One may determine whether a
polypeptide of the invention is likely to be post-translationally
modified by analyzing the sequence of the polypeptide to
determine if there are peptide motifs indicative of sites for
post-translational modification.  There are a number of computer
programs that permit prediction of post-translational
modifications.  See, e.g., ~~www.expasy.org~~ expasy.org of the world
wide web (accessed August 31, 2001), which includes PSORT, for
prediction of protein sorting signals and localization sites,
SignalP, for prediction of signal peptide cleavage sites,
MITOPROT and Predotar, for prediction of mitochondrial targeting
sequences, NetOGlyc, for prediction of type O-glycosylation sites
in mammalian proteins, big-PI Predictor and DGPI, for prediction
of prenylation-anchor and cleavage sites, and NetPhos, for
prediction of Ser, Thr and Tyr phosphorylation sites in
eukaryotic proteins.  Other computer programs, such as those
included in GCG, also may be used to determine post-translational
modification peptide motifs.

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Please replace the paragraph at page 54, lines 20-31, with the

following:

    General examples of types of post-translational

modifications may be found in web sites such as the Delta Mass

database ~~http://www.abrf.org/ABRF/Research~~

~~Committees/deltamass/deltamass.html~~ abrf.org/ABRF/Research

Committees/deltamass/deltamass.html of the world wide

web(accessed October 19, 2001); "GlycoSuiteDB: a new curated

relational database of glycoprotein glycan structures and their

biological sources" Cooper et al. Nucleic Acids Res. 29; 332-335

(2001) and ~~http://www.glycosuite.com/~~ glycosuite.com/ of the

world wide web (accessed October 19, 2001); "O-GLYCBASE version

4.0: a revised database of O-glycosylated proteins" Gupta et al.

Nucleic Acids Research, 27: 370-372  (1999) and

~~http://www.cbs.dtu.dk/databases/OGLYCBASE/~~

http://www.cbs.dtu.dk/databases/OGLYCBASE/ of the world wide

web(accessed October 19, 2001);   "PhosphoBase, a database of

phosphorylation sites: release 2.0.",  Kreegipuu et al. Nucleic

Acids Res 27(1):237-239 (1999) and ~~http://www.cbs.dtu.dk/~~

~~databases/PhosphoBase/~~ cbs.dtu.dk/ databases/PhosphoBase/ of the

world wide web(accessed October 19, 2001); or

~~http://pir.georgetown.edu/ pirwww/search/textresid.html~~

pir.georgetown.edu/ pirwww/search/textresid.html of the world

wide web (accessed October 19, 2001).


Please replace the paragraph at page 56, line 25 through page 57,

line 14, with the following: .

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In another embodiment, the invention provides polypeptides
that have been post-translationally modified.  In one embodiment,
polypeptides may be modified enzymatically or chemically, by
addition or removal of a post-translational modification.  For
example, a polypeptide may be glycosylated or deglycosylated
enzymatically.  Similarly, polypeptides may be phosphorylated
using a purified kinase, such as a MAP kinase (e.g, p38, ERK, or
JNK) or a tyrosine kinase (e.g., Src or erbB2).  A polypeptide
may also be modified through synthetic chemistry.  Alternatively,
one may isolate the polypeptide of interest from a cell or tissue
that expresses the polypeptide with the desired
post-translational modification.  In another embodiment, a
nucleic acid molecule encoding the polypeptide of interest is
introduced into a host cell that is capable of
post-translationally modifying the encoded polypeptide in the
desired fashion. If the polypeptide does not contain a motif for
a desired post-translational modification, one may alter the
post-translational modification by mutating the nucleic acid
sequence of a nucleic acid molecule encoding the polypeptide so
that it contains a site for the desired post-translational
modification.  Amino acid sequences that may be
post-translationally modified are known in the art.  See, e.g.,
the programs described above on the website ~~www.expasy.org~~
expasy.org of the world wide web.  The nucleic acid molecule is
then ~~be~~ introduced into a host cell that is capable of
post-translationally modifying the encoded polypeptide.
Similarly, one may delete sites that are post-translationally
modified by either mutating the nucleic acid sequence so that the
encoded polypeptide does not contain the post-translational

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modification motif, or by introducing the native nucleic acid
molecule into a host cell that is not capable of
post-translationally modifying the encoded polypeptide.


Please replace the paragraph at page 59, line 20 through page 60,
line 2, with the following:

    Plasmid vectors will typically be introduced into chemically
competent or electrocompetent bacterial cells.  *E. coli* cells can
be rendered chemically competent by treatment, *e.g.*, with $CaCl_2$,
or a solution of $Mg^{2+}$, $Mn^{2+}$, $Ca^{2+}$, $Rb^+$ or $K^+$, dimethyl sulfoxide,
dithiothreitol, and hexamine cobalt (III), Hanahan, *J. Mol. Biol.*
166(4):557-80 (1983), and vectors introduced by heat shock.  A
wide variety of chemically competent strains are also available
commercially (e.g., Epicurian Coli® XL10-Gold® Ultracompetent
Cells (Stratagene, La Jolla, CA, USA); DH5α competent cells
(Clontech Laboratories, Palo Alto, CA, USA); and TOP10 Chemically
Competent E. coli Kit (Invitrogen, Carlsbad, CA, USA)).
Bacterial cells can be rendered electrocompetent, that is,
competent to take up exogenous DNA by electroporation, by various
pre-pulse treatments; vectors are introduced by electroporation
followed by subsequent outgrowth in selected media.  An extensive
series of protocols is provided online in Electroprotocols
(BioRad, Richmond, CA, USA)
(http://www.biorad.com/LifeScience/pdf/ New_Gene_Pulser.pdf
biorad.com/LifeScience/pdf/ New_Gene_Pulser.pdf of the world wide
web).

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Please replace the paragraph at page 60, line 25 through page 61,
line 10, with the following:

Mammalian and insect cells can be directly infected by
packaged viral vectors, or transfected by chemical or electrical
means.  For chemical transfection, DNA can be coprecipitated with
$CaPO_4$ or introduced using liposomal and nonliposomal lipid-based
agents.  Commercial kits are available for $CaPO_4$ transfection
(CalPhos™ Mammalian Transfection Kit, Clontech Laboratories, Palo
Alto, CA, USA), and lipid-mediated transfection can be practiced
using commercial reagents, such as LIPOFECTAMINE™ 2000,
LIPOFECTAMINE™ Reagent, CELLFECTIN® Reagent, and LIPOFECTIN®
Reagent (Invitrogen, Carlsbad, CA, USA), DOTAP Liposomal
Transfection Reagent, FuGENE 6, X-tremeGENE Q2, DOSPER, (Roche
Molecular Biochemicals, Indianapolis, IN USA), Effectene™,
PolyFect®, Superfect® (Qiagen, Inc., Valencia, CA, USA).
Protocols for electroporating mammalian cells can be found online
in Electroprotocols (Bio-Rad, Richmond, CA, USA)
((~~http://www.bio-rad.com/LifeScience/pdf/New_Gene_Pulser.pdf~~ see
biorad.com/LifeScience/pdf/New_Gene_Pulser.pdf on the world wide
web); Norton et al. (eds.), Gene Transfer Methods: Introducing
DNA into Living Cells and Organisms, BioTechniques Books, Eaton
Publishing Co. (2000); incorporated herein by reference in its
entirety.  Other transfection techniques include transfection by
particle bombardment and microinjection.  See, e.g., Cheng et
al., Proc. Natl. Acad. Sci. USA 90(10): 4455-9 (1993); Yang et
al., Proc. Natl. Acad. Sci. USA 87(24): 9568-72 (1990).

Please insert the following paragraphs at page 119, line 39:

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**Example 1a: Suppression subtractive hybridization (Clontech PCR-SELECT)**

Clontech PCR-SELECT is a PCR based subtractive hybridization method designed to selectively enrich for cDNAs corresponding to mRNAs differentially expressed between two mRNA populations (Diatchenko et al, *Proc. Natl. Acad. Sci. USA*, Vol. 93, pp. 6025-6030, 1996).

Clontech PCR-SELECT is a method for enrichment of differentially expressed mRNAs based on a selective amplification. cDNA is prepared from the two mRNA populations which are to be compared (Tester: cDNA population in which the differentially expressed messages are sought and Driver: cDNA population in which the differentially expressed transcripts are absent or low). The tester sample is separated in two parts and different PCR adapters are ligated to the 5' ends. Each tester is separately annealed to excess driver (first annealing) and then pooled and again annealed (second annealing) to excess driver. During the first annealing, sequences common to both populations anneal. Additionally the concentration of high and low abundance messages are normalized since annealing is faster for abundant molecules due to the second order kinetics of hybridization. During the second annealing cDNAs unique or overabundant to the tester can anneal together. Such molecules have different adapters at their ends. The addition of additional driver during the second annealing enhances the enrichment of the desired differentially expressed sequences. During subsequent PCR, molecules that have different adapters at each end amplify exponentially. Molecules which have identical adapters, or adapters at only one end, or no adapters (driver

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sequences) either do not amplify or undergo linear amplification. The end result is enrichment for cDNAs corresponding to differentially expressed messages (unique to the tester or upregulated in the tester). This technique was used to identify transcripts unique to prostate tissues or messages overexpressed in prostate cancer tissues.

Pairs of matched samples were isolated from the same patient, a cancer sample, and the "normal" adjacent tissue from the same tissue type. The mRNA from the cancer tissue was used as the "tester", and the non-cancer mRNA as a "driver". The non-cancer "driver" is from the same individual and tissue as the cancer sample (Matched). Alternatively, the "driver" can be from a different individual but the same tissue as the tumor sample (unmatched). In some cases "driver" mixtures of mRNAs derived from non-cancer tissues types different from the cancer tissue type are used. The last approach allows the identification of transcripts whose expression is specific or upregulated in the cancer tissue type analyzed. Such transcripts may or may not be cancer specific in their expression.

Several subtracted libraries were generated for prostate tissue. The product of the subtraction experiments was used to generate cDNA libraries. These cDNA libraries contain Expressed Sequence Tags (ESTs) from genes that are prostate specific, or upregulated in prostate tissue. Randomized clones picked from each cDNA PCR Select library were sequenced and the genes identified by a systematic analysis of the sequence data against the LIFESEQ Gold database available from Incyte Pharmaceuticals, Palo Alto. The sequences with no significant homology to any DNA sequence present in the database are considered novel sequences.

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These prostate cancer specific markers are DEX0128_1 through DEX0128_100 and correspond to markers of the instant sequence listing as depicted in the table in Example 1.

Please replace the paragraph at page 124, line 46 through page 125, line 2 with the following:

Examples of post-translational modifications (PTMs) of the ~~BSPs~~ PSPs of this invention are listed below.  In addition, antibodies that specifically bind such post-translational modifications may be useful as a diagnostic or as therapeutic. Using the ProSite database (Bairoch et al., Nucleic Acids Res. 25(1):217-221 (1997), the contents of which are incorporated by reference), the following PTMs were predicted for the ~~LSPs~~ PSPs of the invention (~~http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_prosite.html~~ npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_prosite.html of the world wide web, most recently accessed October 23, 2001). For full definitions of the PTMs see ~~http://www.expasy.org/cgi-bin/prosite-list.pl~~ expasy.org/cgi-bin/prosite-list.pl of the world wide web, most recently accessed October 23, 2001.